

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 6, 2005, 06:11:39 ; Search time 93 Seconds
(without alignments)
897.515 Million cell updates/sec

Title: US-10-616-410-2

Perfect score: 852

Sequence: 1 MADEKLPWCKRMRSRG.....GEMSGPVFTDSGIHILRTE 163

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03.*

1: uniprot_prot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance, to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	852	100.0	163	1	PIN1_HUMAN	Q13526 homo sapien
2	814	95.5	165	1	PIN1_MOUSE	Q9qur7 mus musculu
3	753	88.4	159	2	Q919K6	Q919K6 xenopus lae
4	752	88.3	159	2	Q642N3	Q642N3 xenopus tro
5	751	88.1	159	2	Q6DEE1	Q6DEE1 xenopus lae
6	748	87.8	158	2	Q6AZR5	Q6AZR5 xenopus lae
7	681	79.9	159	2	Q6FBX1	Q6pbi1 brachydanio
8	491	57.6	191	2	Q7QAB6	Q7qab6 anopheles g
9	456.5	53.6	166	1	DOD DROME	P54353 drosophila
10	436	51.2	168	2	Q9N492	Q9N492 caenorhabdi
11	433.5	50.9	186	2	Q7RVY7	Q7rvy7 neurospora
12	428.5	50.3	182	1	SSP1_NEUCR	Q60045 neurospora
13	408.5	47.9	190	2	Q6UAY2	Q6uay2 paracoccidi
14	397	46.6	176	2	Q42735	Q42735 emericeella
15	388.5	45.6	175	1	PIN1_SCHPO	Q44448 schizosacch
16	387	45.4	185	2	Q6CEL8	Q6cel8 yarrowia li
17	370	43.4	162	2	Q6CMZ3	Q6cmz3 kluyveromyc
18	369.5	43.4	177	2	Q9CA75	Q9ca75 candida alb
19	364	42.7	178	2	Q8NUN5	Q8nunj5 cryptococcu
20	360	42.3	177	2	Q6BRV8	Q6brv8 debaryomyce
21	356.5	41.8	190	1	ES51_YEAST	P22696 saccharomyc
22	352	41.3	173	2	Q6FXP9	Q6fxp9 candida gla
23	351.5	41.3	243	2	P90527	P90527 dictyosteli
24	341	40.0	163	2	Q7SCN9	Q7scn9 ashbya gos
25	338	39.7	148	2	Q7QAB7	Q7qab7 anopheles g
26	301	35.3	119	1	PIN1_ARATH	Q98142 arabidopsis
27	297	34.9	100	1	PIN1_HUMAN	O15428 homo sapien
28	296.5	34.8	121	1	PIN1_NALDO	Q94900 malus domes
29	283	33.2	118	1	PIN1_DICLA	Q9lek8 digitalis l
30	280	32.9	123	2	Q7XTK0	Q7xtk0 oryza sativ
31	277	32.5	386	2	Q8IRJ5	Q8irj5 drosophila

Q8SR85 encephalito
Q6mr41 bdellovibri
Q72d64 desulfovibr
Q82au8 nitrosomona
Q74bg7 geobacter s
Q899g4 clostridium
P24327 bacillus su
Q74049 cenarchaeum
Q97mb9 clostridium
Q74ae7 geobacter s
Q6eek5 oryza sativ
Q6gsul bartonella
Q65lt4 bacillus li
Q6g0q7 bartonella

ALIGNMENTS

RESULT 1
ID PIN1_HUMAN STANDARD; PRT; 163 AA.
AC Q13526;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DE 25-OCT-2004 (Rel. 45, Last annotation update)
DE Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1 (EC 5.2.1.8)
DE (Rotamase Pin1) (PPIase Pin1).
GN Name=PIN1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96195064; PubMed=8606777; DOI=10.1038/380544a0;
RA Lu K.P., Hanes S.D., Hunter T.;
RT "A human peptidyl-prolyl isomerase essential for regulation of
RT mitosis."
RL Nature 380:544-547 (1996).
RN [2]
RP SEQUENCE FROM N.A.

RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Boesak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Heltom E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Griewood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RN [3]
RP Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RP X-RAY CRYSTALLOGRAPHY (1.35 ANGSTROMS).
RX MEDLINE=97344079; PubMed=9200606; DOI=10.1016/S0092-8674(00)80273-1;
RA Ranganathan R., Lu K.P., Hunter T., Noel J.P.;
RT "Structural and functional analysis of the mitotic rotamase Pin1
RT suggests substrate recognition is phosphorylation dependent."
RL Cell 89:875-886 (1997).
CC -!- FUNCTION: Essential PPIase that regulates mitosis presumably by
interacting with NIMA and attenuating its mitosis-promoting

Exhibit F

activity. Displays a preference for an acidic residue N-terminal to the isomerized proline bond. Catalyzing pSer/Thr-Pro cis/trans isomerizations.

-1- CATALYTIC ACTIVITY: Peptidylproline (omega-180) = peptidylproline (omega-0).

-1- SUBCELLULAR LOCATION: Nuclear.

-1- SIMILARITY: Belongs to the pp1c/parvulin rotamase family.

-1- SIMILARITY: Contains 1 WW domain.

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EMBL; U49070; AAC50492.1; --

EMBL; BC002899; AA02899.1; --

PIR; S68520; S68520.

PDB; 1P8A; X-ray; B=1-163.

PDB; 1I6C; NMR; A=6-44.

PDB; 1I8G; NMR; B=6-44.

PDB; 1I8H; NMR; B=6-44.

PDB; 1NMV; NMR; A=1-163.

PDB; 1NMW; NMR; A=50-163.

PDB; 1PIN; X-ray; A=1-163.

Genew; HGNC:8988; PIN1.

H-InvDB; HIX0014730; --

MIM; 601052; --

GO; GO:0005634; C:nucleus; TAS.

GO; GO:0005515; P:protein binding; TAS.

GO; GO:0007088; P:regulation of mitosis; TAS.

InterPro; IPR000297; Rotamase.

InterPro; IPR001202; WW_Rsp5_WWP.

Pfam; PF00639; Rotamase_1.

Pfam; PF00397; WW; 1.

SMART; SM00456; WW; 1.

PROSITE; PS01096; PPIC_PPIASE_1; 1.

PROSITE; PS01198; PPIC_PPIASE_2; 1.

PROSITE; PS01159; WW_DOMAIN_1; 1.

PROSITE; PS00020; WW_DOMAIN_2; 1.

3D-structure; Cell cycle; Isomerase; Nuclear protein; Rotamase.

DOMAIN 5 39

DOMAIN 52 163

DOMAIN 9 10

DOMAIN 11 15

DOMAIN 17 18

DOMAIN 22 26

DOMAIN 27 29

DOMAIN 32 33

DOMAIN 55 62

DOMAIN 65 66

DOMAIN 72 72

DOMAIN 73 74

DOMAIN 75 75

DOMAIN 82 98

DOMAIN 99 99

DOMAIN 103 110

DOMAIN 114 118

DOMAIN 119 120

DOMAIN 121 125

DOMAIN 127 128

DOMAIN 132 140

DOMAIN 143 144

DOMAIN 146 146

DOMAIN 150 151

DOMAIN 156 161

SEQUENCE 163 AA; 18243 MW; 35391AP40B7D1E13 CRC64;

Query Match

Best Local Similarity 100.0%; Score 852; DB 1; Length 163;

Matches 163; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MADEEKLPPGWKRMSSSSGRVYFNHITNASOWERPSSGSGKNGQGPAPVRCSHL 60
Db 1 MADEEKLPPGWKRMSSSSGRVYFNHITNASOWERPSSGSGKNGQGPAPVRCSHL 60
Qy 61 LVKHSQSRPSSRWQEKITTKKEALELINGYIQIKSGEDPESLASQFSDCSAKARG 120
Db 61 LVKHSQSRPSSRWQEKITTKKEALELINGYIQIKSGEDPESLASQFSDCSAKARG 120
Qy 121 DLGAFSGQKQKPEDASPALRTGEMSGPVFTDGIHILRTE 163
Db 121 DLGAFSGQKQKPEDASPALRTGEMSGPVFTDGIHILRTE 163

RESULT 2

PIN1_MOUSE STANDARD; PRT; 165 AA.
AC Q90U7;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, last sequence update)
DT 05-JUL-2004 (Rel. 44, last annotation update)
DE Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1 (BC 5.2.1.8)
DE (Rotamase Pin1) (PPIase Pin1).
GN Name=Pin1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20070807; PubMed=10600477; DOI=10.1006/bbrc.1999.1736;
RA Fujimori F., Takahashi K., Uchida C., Uchida T.;
RT "Mice lacking Pin1 develop normally, but are defective in entering
cell cycle from G0 arrest."
RL Biochem. Biophys. Res. Commun. 265:658-663(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CS7BL/6J; TISSUE=Embryo, and Kidney;
RX MEDLINE=22354683; PubMed=12468851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaide I., Osato N., Saito R., Suzuki H., Yamana H., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojohori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Bruscia V., Chochia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.P., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlstedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
CC -!- FUNCTION: Essential PPIase that regulates mitosis presumably by
interacting with NIMA and attenuating its mitosis-promoting
activity. Displays a preference for an acidic residue N-terminal
to the isomerized proline bond. Catalyzing pSer/Thr-Pro cis/trans
isomerizations (By similarity).

Science 287:1644-1647(2000).

CC -1- SIMILARITY: Belongs to the ppiC/parvulin rotamase family.

DR RBL; AF239760; AAF43897.1; -.

DR HSP; Q13526; 1P8A.

DR GO; GO:0016853; F:isomerase activity; IEA.

DR GO; GO:0003755; F:peptidyl-prolyl cis-trans isomerase activity; IEA.

DR GO; GO:0006457; P:protein folding; IEA.

DR InterPro; IPR000297; Rotamase.

DR InterPro; IPR002349; WW.

DR InterPro; IPR001202; WW_Rep5_WWP.

DR Pfam; PF006639; Rotamase; 1.

DR Pfam; PF003397; WW; 1.

DR PRINTS; PR00403; WWDOMAIN.

DR SMART; SM00456; WW; 1.

DR PROSITE; PS01096; PPIC_PPIASE_1; 1.

DR PROSITE; PS01198; PPIC_PPIASE_2; 1.

DR PROSITE; PS01159; WW_DOMAIN_1; 1.

DR PROSITE; PS00020; WW_DOMAIN_2; 1.

KW isomerase; Rotamase.

QY SEQUENCE 159 AA; 17671 MW; 4B54F66F16C9DF1C CRC64;

Query Match 88.4%; Score 753; DB 2; Length 159;

Best Local Similarity 87.1%; Pred. No. 3.6e-61;

Matches 142; Conservative 11; Mismatches 6; Indels 4; Gaps 1

QY 1 MADEEKLPPGWEXKMRSSGRVYFNHITNASQWRPSSGGKNGQGBPARVRCSHL 60

DB 1 MADEEKLPPGWEXKMRSSGRVYFNHITNASQWERP----IAGGKNGQGBPKVRCSHL 56

QY 61 LVKHSQRRSSRWQEKITTKKEALELINGYIOKIKSGEDFESLASQFDCSSAKAG 120

DB 57 LVKHSQRRSSRWQDKITTSKQALELINGYIOKMSGDFESLASQFDCSSAKAGG 116

QY 121 DLGAFSGMQKQPEDASFALRTGEMSGPVFTDSGIHILATE 163

DB 117 DLGSGFGKMQKQPEDASFALRPGEMSGPVFTDSGIHILATE 159

RESULT 4

Q642N3 PRELIMINARY; PRT; 159 AA.

ID Q642N3

AC Q642N3, 2004 (TrEMBLrel. 28, Created)

DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)

DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)

DE Hypothetical protein.

OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;

OC Xenopodinae; Xenopus.

OX NCBI_TaxID=8364;

FP [1]

RN SEQUENCE FROM N.A.

RP TISSUE=Embryo;

KC PubMed=12477932; DOI=10.1073/pnas.242603899;

RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,

RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahy J., Halton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting J.M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzywinski M.I., Skalek U., Smallus D.B., Schnerch A., Schein J.E.,

RA Jones S.J., Marra M.A.

RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RM [2]
 RC SEQUENCE FROM N.A.

RP TISSUE=Embryo;
 RA Klein S., Gerhard D.S.; to the EMBL/GenBank/DBJ databases.
 RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC081312; AAH81312.1; -
 KW Hypothetical protein.

SQ SEQUENCE 159 AA; 17793 MW; AL7A9C6C0B0A858 CRC64;
 Query Match 88.3%; Score 752; DB 2; Length 159;
 Best Local Similarity 87.1%; Pred. No. 4.4e-61;
 Matches 142; Conservative 11; Mismatches 6; Indels 4; Gaps 1;

QY 1 MADEKLPFGWEKMSRSSGRVYFNHITNASQWERPSGSGKNGQGEFARVRCSHL 60
 DB 1 MADEKLPFGWEKMSRSSGRVYFNHITNASQWERP-----TTGGKNGQGEFARVRCSHL 56
 QY 61 LVKHSQSRPPSSWRQEKITRTKEALELINGYIQIKSGDEDFESLASQFSDCSAKARG 120
 DB 57 LVKHSQSRPPSSWRQDRITRTKDEALELINGYIQIKSGDEDFESLASQFSDCSAKAGG 116

QY 121 DLGAFSGQWQKPPEDASFALETCGMSGPVFTDSGIHILRTE 163
 DB 117 DLGSGFGKAMQKPPEDASFALETCGMSGPVFTDSGIHILRTE 159

RESULT 5
 Q6AEZ5 PRELIMINARY; PRT; 159 AA.

AC Q6AEZ5
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Hypothetical protein.

OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
 OC Xenopodinae; Xenopus.

OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.

RC TISSUE=Embryo;
 RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.B.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley D.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences."

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RM [3]
 RC SEQUENCE FROM N.A.

RP TISSUE=Embryo;
 RA Klein S., Strausberg R.; to the EMBL/GenBank/DBJ databases.
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the pPic/parvulin rotamase family.
 DR EMBL; BC077181; AAH77181.1; -
 KW Hypothetical protein.

SQ SEQUENCE 159 AA; 17641 MW; C8CF4A870E316D3B CRC64;
 Query Match 88.1%; Score 751; DB 2; Length 159;
 Best Local Similarity 86.5%; Pred. No. 5.4e-61;
 Matches 141; Conservative 12; Mismatches 6; Indels 4; Gaps 1;

QY 1 MADEKLPFGWEKMSRSSGRVYFNHITNASQWERPSGSGKNGQGEFARVRCSHL 60
 DB 1 MADEKLPFGWEKMSRSSGRVYFNHITNASQWERP-----TAGGKNGQGEFARVRCSHL 56
 QY 61 LVKHSQSRPPSSWRQEKITRTKEALELINGYIQIKSGDEDFESLASQFSDCSAKARG 120
 DB 57 LVKHSQSRPPSSWRQDNITRTKDEALELINGYIQIKSGDEDFESLASQFSDCSAKAGG 116

QY 121 DLGAFSGQWQKPPEDASFALETCGMSGPVFTDSGIHILRTE 163
 DB 117 DLGSGFGKAMQKPPEDASFALETCGMSGPVFTDSGIHILRTE 159

RESULT 6
 Q6AEZ5 PRELIMINARY; PRT; 158 AA.

AC Q6AEZ5
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Hypothetical protein (fragment).

OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
 OC Xenopodinae; Xenopus.

OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.

RC TISSUE=Lung;
 RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.B.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley D.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences."

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalhus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RC Klein S., Strausberg R.;
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the pp1C/parvulin rotamase family.
 DR EMBL; BC077447; AH77447.1; -;
 DR GO; GO:0016953; F:isomerase activity; IEA.
 DR InterPro; IPR000297; Rotamase.
 DR InterPro; IPR002349; WW.
 DR InterPro; IPR001202; WW_Rep5_WWP.
 DR Pfam; PF00639; Rotamase; 1.
 DR Pfam; PF00397; WW; 1.
 DR PRINTS; PR00403; WWDOMAIN.
 DR SMART; SM00456; WW; 1.
 DR PROSITE; PS01096; PPIC_PPIASE_1; 1.
 DR PROSITE; PS01198; PPIC_PPIASE_2; 1.
 DR PROSITE; PS01159; WW_DOMAIN_1; 1.
 DR PROSITE; PS01159; WW_DOMAIN_2; 1.
 DR PROSITE; PS0020; WW_DOMAIN_2; 1.
 DR Hypothetical protein; Isomerase; Rotamase.
 KW NON TER 1
 FT 1
 SQ SEQUENCE 158 AA; 17539 MW; EB4FF9F7650FFA1 CRC64;
 Query Match 87.8%; Score 748; DB 2; Length 158;
 Best Local Similarity 87.0%; Pred. No. 1e-60;
 Matches 141; Conservative 11; Mismatches 6; Indels 4; Gaps 1;
 QY 2 ADEKLPPGWEKMSRSGRVYFNHITNASQWERPSGNSGGKNGQGEPARVRCSHLL 61
 DB 1 ADEKLPPGWEKMSRSGRVYFNHITNASQWERP-----IAGKNGQGEPPGKVRCSHLL 56
 QY 62 VKHSQSRPPSSWRQEKITRTKEALELINGYIQIKSGEEDFESLASQFDCSSAKARG 121
 DB 57 VKHNSRRPSSWRQDKITRSKDEALQLQIKYIEQIKSGEEDFESLASQFDCSSAKARG 116
 QY 122 LGAFSGQKQKPPEDASFAALTGTGMSGPVFTDGIHILRT 163
 DB 117 LGSFGKGMQKPPEDASFAALPGMSGPVFTDGIHILRT 158
 RESULT 7
 Q6P6X1 PRELIMINARY; PRT; 159 AA.
 AC Q6P6X1;
 DT 05-JUL-2004 (Tremblrel. 27, Created)
 DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
 DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
 DE Hypothetical protein zgc:73206;
 GN ORFNames=zgc:73206;
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OC NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Wild-type; TISSUE=Eye;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zebberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalhus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Wild-type; TISSUE=Eye;
 RC Strausberg R.;
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the pp1C/parvulin rotamase family.
 DR EMBL; BC059553; AAH59553.1; -;
 DR ZFIN; ZDB-GENE-040426-1714; zgc:73206.
 DR GO; GO:0016953; F:isomerase activity; IEA.
 DR GO; GO:0003755; P:peptidyl-prolyl cis-trans isomerase activity; IEA.
 DR GO; GO:0006457; P:protein folding; IEA.
 DR InterPro; IPR000297; Rotamase.
 DR InterPro; IPR001202; WW_Rep5_WWP.
 DR Pfam; PF00639; Rotamase; 1.
 DR Pfam; PF00397; WW; 1.
 DR SMART; SM00456; WW; 1.
 DR PROSITE; PS01096; PPIC_PPIASE_1; 1.
 DR PROSITE; PS01198; PPIC_PPIASE_2; 1.
 DR PROSITE; PS01159; WW_DOMAIN_1; 1.
 DR PROSITE; PS01159; WW_DOMAIN_2; 1.
 KW Hypothetical protein; Isomerase; Rotamase.
 SQ SEQUENCE 159 AA; 17706 MW; 1A836D6259D8B718 CRC64;
 Query Match 79.9%; Score 681; DB 2; Length 159;
 Best Local Similarity 79.0%; Pred. No. 1.4e-54;
 Matches 128; Conservative 17; Mismatches 13; Indels 4; Gaps 1;
 QY 1 MADEKLPPGWEKMSRSGRVYFNHITNASQWERPSGNSGGKNGQGEPARVRCSHL 60
 DB 1 MSDDEKLPSGWEKMSRSGRVYFNHITNASQWERPSG-----GADGAGDVKEKRCSHL 56
 QY 61 LVKHSQSRPPSSWRQEKITRTKEALELINGYIQIKSGEEDFESLASQFDCSSAKARG 120
 DB 57 LVKHSQSRPPSSWRREENITRSKDEALQLQIKYIEQIKSGEEDFESLASQFDCSSAKARG 116
 QY 121 DLGAFSGQKQKPPEDASFAALTGTGMSGPVFTDGIHILRT 162
 DB 117 DLGLFGRGQKQKPPEDASFAALPGMSGPVFTDGIHILRT 158
 RESULT 8
 Q7QAB6 PRELIMINARY; PRT; 191 AA.
 ID Q7QAB6
 AC Q7QAB6;
 DT 01-MAR-2004 (Tremblrel. 26, Created)
 DT 01-MAR-2004 (Tremblrel. 26, Last sequence update)
 DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
 DE AGCP13948 (Fragment).
 GN Name=agc50456; ORFNames=ENSANGG00000011536;
 OS Anopheles gambiae str. PEST.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
 OC NCBI_TaxID=180454;
 RN [1]
 RP SEQUENCE FROM N.A.

DR Pfam; PF00639; Rotamase; 1.
 DR Pfam; PF00397; WW; 1.
 DR SMART; SM00456; WW; 1.
 DR PROSITE; PS01096; PPIC_PPIASE_1; 1.
 DR PROSITE; PS01098; PPIC_PPIASE_2; 1.
 DR PROSITE; PS01159; WW_DOMAIN_1; 1.
 DR PROSITE; PS01159; WW_DOMAIN_2; 1.
 KW Isomerase; Rotamase.
 FT DOMAIN 5 39 WW.
 FT DOMAIN 55 166 PpIC.
 FT CONFLICT 44 44 A -> T (in Ref. 2).
 SQ SEQUENCE 166 AA; 18376 MW; 3B4306FA930E7259 CRC64;

Query Match 53.6%; Score 456.5; DB 1; Length 166;
 Best Local Similarity 56.7%; Pred. NO. 6.2e-34;
 Matches 93; Conservative 16; Mismatches 52; Indels 3; Gaps 2;

QY 1 MADEEKLPGWEKMSRSSGRVYFNHITNASQWERPS--GNSSGGKNGQGE-PARVRC 57
 DB 1 MPDAQLPGWEKMSRSSGRVYFNHITNASQWERPS--GNSSGGKNGQGE-PARVRC 60

QY 58 SHLLVKHSOSRPPSSWRQEKTRTKKEALELINGYIKIKSGEEDPFESLASOFDCSSAK 117
 DB 61 LHLVVKHSOSRPPSSWRQEKTRTKKEALELINGYIKIKSGEEDPFESLASOFDCSSAK 120

QY 118 ARGDLAGSRGQMQPFDASPAITGEMSGVPFTDSGHIILR 161
 DB 121 RGGDLGKGRGQMAAFDAEAFKLVNQLSGIVSDSGLHIILR 164

RESULT 10

Q9N492 PRELIMINARY; PRT; 168 AA.

AC Q9N492;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical protein Y110A2AL.13;
 GN Name=Y110A2AL.13; ORFNames=Y110A2AL.13;
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RG WormBase Consortium;
 RT "Genome sequence of the nematode C. elegans: a platform for
 RL investigating biology. The C. elegans Sequencing Consortium.";
 RL Science 282:2012-2018(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Smith A.;
 RT "The sequence of C. elegans cosmid Y110A2AL.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Waterston R.H.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Waterston R.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Waterston R.;
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 RN [6]

RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Waterston R.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Waterston R.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 RN [8]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Waterston R.;
 RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
 RN [9]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Waterston R.;
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
 RN [10]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Waterston R.;
 RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
 RN [11]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Waterston R.;
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 RN [12]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Waterston R.;
 RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
 RN [13]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Wilson R.;
 RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
 RN [14]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Wilson R.;
 RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
 RN [15]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RG WormBase Consortium;
 RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the pp1C/parvulin rotamase family.
 DR EMBL; AC024746; AAF60409.1; -.
 DR HSP; Q13526; 1PIN.
 DR WormBase; WBGene0022448; Y110A2AL.13.
 DR WormPep; Y110A2AL.13; CE25189.
 DR GO; GO:0016853; F:isomerase activity; IEA.
 DR InterPro; IPR000297; Rotamase.
 DR InterPro; IPR001202; WW_Rsp5_WWP.
 DR Pfam; PF00639; Rotamase; 1.
 DR Pfam; PF00397; WW; 1.
 DR SMART; SM00456; WW; 1.
 DR PROSITE; PS01098; PPIC_PPIASE_2; 1.
 DR PROSITE; PS01159; WW_DOMAIN_1; 1.
 DR PROSITE; PS01159; WW_DOMAIN_2; 1.
 KW Hypothetical protein; Isomerase; Rotamase.
 SQ SEQUENCE 168 AA; 19176 MW; 0FC837780579C070 CRC64;

Query Match 51.2%; Score 436; DB 2; Length 168;
 Best Local Similarity 54.8%; Pred. NO. 4.8e-32;
 Matches 92; Conservative 17; Mismatches 45; Indels 14; Gaps 4;

QY 4 EEKLPGWKEKMSRSSGRVYFNHITNASQWERPSGNSGGKNGQGE-PARVRCSHLLVK 63
 DB 3 DNSLPAGWKEKMSRSSGRVYFNHITNASQWERPSGNSGGKNGQGE-PARVRCSHLLVK 58

QY 64 HQSRPSSRWQEKITRTKEALELING-----YIQIKSG---BEDFSLASQFSDC 113
 DB 59 HDGSRNPSSWRGHDITRSKODAINILKSADLRNFHYEKELKODASNIIEGKFRILAKQFSDC 118
 QY 114 SSKARGDILGASRGOMQKPFEDASPALRTGEMSGPVFTDSDGIHILR 161
 DB 119 SSKARGDILGPPERRQMOKPFEDASPALRTGEMSGDIVDTSSGVHILYR 166

RESULT 11

QY 01-MAR-2004 (TREMELrel. 26, Created)
 DB 01-MAR-2004 (TREMELrel. 26, Last sequence update)
 QY 01-MAR-2004 (TREMELrel. 26, Last annotation update)
 DB 01-MAR-2004 (TREMELrel. 26, Last annotation update)
 DE Hypothetical protein (AJ006023) peptidylprolyl isomerase).
 GN Name=NCU08554.1;
 OS Neurospora crassa.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
 OX NCBI_TaxID=5141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=OR74A;
 RA Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
 RA Jaffe D., FitzHugh W., Wang L.-J., Smirnov S., Purcell S., Rehman B.,
 RA Elkins T., Engels R., Ma S., Nielsen C.B., Butler J., Endrizzi M.,
 RA Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,
 RA Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zeiter A., Schulte U.,
 RA Kothe G.O., Jedd G., Meves W., Staben C., Marcotte E., Greenberg D.,
 RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
 RA Kamal M., Kamysysselis M., Mauceli E., Bielke C., Rudd S., Frishman D.,
 RA Kryatofova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S.,
 RA Cogoni C., Macino G., Catcheside D., Li W., Pratt R.J., Omani S.A.,
 RA DeSouza C.C., Glaes L., Orbach M.J., Berglund J., Voelker R.,
 RA Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
 RA Natvig D.O., Alex L.A., Manhaupt G., Ebbole D.J., Freitag M.,
 RA Paulsen I., Sachs M.S., Lander E.S., Nussbaum C., Birren B.,
 RA "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
 RL Nature 0-0-0(2003)
 CC -!- SIMILARITY: Belongs to the ppiC/parvulin rotamase family.
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AABX01000166; EAA33800.1; -;
 DR HSSP; Q13526; 1P8A.
 DR GO; GO:0016853; Frisomerase activity; IEA.
 DR GO; GO:0003755; P:peptidyl-prolyl cis-trans isomerase activity; IEA.
 DR GO; GO:0006457; P:protein folding; IEA.
 DR InterPro; IPR000297; Rotamase.
 DR InterPro; IPR001202; WW_Rsp5_WWP.
 DR Pfam; PF00639; Rotamase; 1.
 DR Pfam; PF00397; WW; 1.
 DR PROSITE; PS50198; PPII PPIASE 2; 1.
 DR PROSITE; PS01159; WW DOMAIN 1; 1.
 DR PROSITE; PS50020; WW DOMAIN 2; 1.
 KW Hypothetical protein; Isomerase; Rotamase.
 SQ SEQUENCE 186 AA; 21175 MW; B8E214B1B01AEA36 CRC64;

Query Match 50.9%; Score 433.5; DB 2; Length 186;
 Best Local Similarity 51.1%; Pred. No. 9.2e-32;
 Matches 91; Conservative 20; Mismatches 50; Indels 17; Gaps 2;

QY 1 MADEKLPQWKEKMSRSGRVYFNHITNASQWERPSG-----NSSSG 44
 DB 1 MTETGLPDEWVRHSQSKNLPYFNATKTSRWPEPSGTVDVKLIYMAKHSPTSQQQ 60
 QY 45 GNGQGEPE-ARVCSHLVKSQSRPSSRWQEKITRTKEALELINGYIQIKSGEEDF 103
 DB 61 QQQQQQPOGKIRCAHLVKNQSRPSSRWSEITRTKEALTTLQGFQRIKSGISL 120

QY 104 ESLASQFDCSSAKARGDILGAFSGOMQKPFEDASPALRTGEMSGPVFTDSDGIHILR 161
 DB 121 GELALTESDCSSARRKRGDLYFGRGDMQKBEDAAFAALKPGEISIVDTASGLHLIER 178

RESULT 12

QY SSPI_NEUCR
 DB ID SSPI_NEUCR STANDARD; PRT; 182 AA.
 AC O60045;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Peptidyl-prolyl cis-trans isomerase sspl (EC 5.2.1.8) (PPIase sspl).
 GN Name=sspl-1;
 OS Neurospora crassa.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
 OX NCBI_TaxID=5141;
 RN [1]
 RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
 RX MEDLINE=99041963; PubMed=9822668; DOI=10.1074/jbc.273.48.31971;
 RA Kops O., Eckerskorn C., Hottenrott S., Fischer G., Mi H.,
 RA Tropschug M.;
 RT "Sspl, a site specific parvulin homolog from N.crassa active in
 RT protein folding.";
 RL J. Biol. Chem. 273:31971-31976(1998).
 CC -!- FUNCTION: Site-specific PPIase with respect to the amino acid N-
 CC terminal to the proline residue. Peptides with glutamate,
 CC phosphoserine, or phosphothreonine in the -1 position are the best
 CC substrates. It is not only able to isomerize small peptides but is
 CC also active in protein folding.
 CC -!- CATALYTIC ACTIVITY: Peptidylproline (omega=180) = peptidylproline
 CC (omega=0).
 CC -!- SIMILARITY: Belongs to the ppiC/parvulin rotamase family.
 CC -!- SIMILARITY: Contains 1 WW domain.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL; AJ006023; CAA06818.1; -;
 DR HSSP; Q13526; 1P8A.
 DR InterPro; IPR000297; Rotamase.
 DR InterPro; IPR001202; WW_Rsp5_WWP.
 DR Pfam; PF00639; Rotamase; 1.
 DR Pfam; PF00397; WW; 1.
 DR SMART; SM00456; WW; 1.
 DR PROSITE; PS50198; PPII PPIASE 2; 1.
 DR PROSITE; PS01159; WW DOMAIN 1; 1.
 DR PROSITE; PS50020; WW DOMAIN 2; 1.
 KW Isomerase; Rotamase.
 FT DOMAIN 7 41 WW.
 FT DOMAIN 60 71 Gln-rich.
 FT DOMAIN 71 182 PpiC.
 SQ SEQUENCE 182 AA; 20673 MW; ACBD0497DFFF7339 CRC64;

Query Match 50.3%; Score 428.5; DB 1; Length 182;
 Best Local Similarity 50.8%; Pred. No. 2.6e-31;
 Matches 90; Conservative 20; Mismatches 50; Indels 17; Gaps 2;

QY 4 EEKLPQWKEKMSRSGRVYFNHITNASQWERPSG-----NSSSGKN 47
 DB 6 ETGLPDEWVRHSQSKNLPYFNATKTSRWPEPSGTVDVKLIYMAKHSPTSQQQQ 65
 QY 48 GQGEPE-ARVCSHLVKSQSRPSSRWQEKITRTKEALELINGYIQIKSGEEDF 106
 DB 66 QQQQPOGKIRCAHLVKNQSRPSSRWSEITRTKEALTTLQGFQRIKSGISL 125
 QY 107 ASQFDCSSAKARGDILGAFSGOMQKPFEDASPALRTGEMSGPVFTDSDGIHILR 163


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Db 126 ALTESDCSARKRGDLGFGMDQKPEFADAFALKPGESISDVDPASGLHLIERLE 182
RESULT 13
Q6UAY2 PRELIMINARY; PRT; 190 AA.
AC Q6UAY2;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Peptidyl-prolyl cis/trans isomerase.
OS Paracoccidioides brasiliensis.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Oxygenales; Mitosporic Oxygenales; Paracoccidioides.
OX NCBI_TaxID=121759;
RN [1]
RP SEQUENCE FROM N.A.
RA Domingos P.C., Pereira M., Castro N.S., Felipe M.S.S., Soares C.M.A.,
RA Jesuino R.S.A.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the pp1c/parvulin rotamase family.
DR EMBL; AY374446; AAC83700.1; -.
DR GO; GO:0016853; P:isomerase activity; IEA.
DR GO; GO:0003755; P:peptidyl-prolyl cis-trans isomerase activity; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR InterPro; IPR000297; Rotamase.
DR InterPro; IPR001202; WW_Rsp5_WMP.
DR Pfam; PF00639; Rotamase; 1.
DR Pfam; PF00397; WW; 1.
DR SMART; SM00456; WW; 1.
DR PROSITE; PS0198; PPIC_PPIASE_2; 1.
DR PROSITE; PS01159; WW_DOMAIN_1; 1.
DR PROSITE; PS0020; WW_DOMAIN_2; 1.
KW Isomerase; Rotamase.
SQ SEQUENCE 190 AA; 20983 MW; 710DCBEFAA9238AE CRC64;

Query Match 47.9%; Score 408.5; DB 2; Length 190;
Best Local Similarity 44.9%; Pred. No. 1.9e-29;
Matches 83; Conservative 24; Mismatches 53; Indels 25; Gaps 1;

QY 4 EEKLPQGEKMSRSGRVVYFNHITNASQWERPSGNS----- 41
Db 6 ETGLSGVEVHSNKNLPYFNPTATRESRWEPPDNTTEKLKYNMAQHSLAERNNA 65
QY 42 ---SSGKNGQGEPARVRCSHLLVKHSQSRPSRWQEKITRKEALELINGYIQIKS 98
Db 66 TGVTSAGVSSADGKIRASHLLIKHQSRRPSSRWREAITRKEALEILRRHESIRS 125
QY 99 GEEDFESLASQFDCSSAKARGDLGAFSGQMKPFEDASPALRTGEMSGPVFTDGIHI 158
Db 126 GEKTLGDIAMSBDSCSARKRGDLGFGFGEMQAEFEEAFAALPQGVSGIVETASGVHL 185
QY 159 ILRTE 163
Db 186 IERLQ 190

RESULT 14
O42735 PRELIMINARY; PRT; 176 AA.
AC O42735;
DT 01-JUN-1998 (TReMBLrel. 06, Created)
DT 01-JUN-1998 (TReMBLrel. 06, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Peptidyl-prolyl cis/trans isomerase.
GN Name=pin1;
OS Emericella nidulans (Aspergillus nidulans).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; Emericella.
OX NCBI_TaxID=162425;
RN [1]
RP SEQUENCE FROM N.A.

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RC STRAIN-R153;
RX MEDLINE=98151356; PubMed=9482729; DOI=10.1093/emboj/17.5.1315;
RA Crenshaw D.G., Yang J., Means A.R., Kornbluth S.;
RT "The mitotic peptidyl-prolyl isomerase, Pin1, interacts with Cdc25 and
RT Plx1.";
RL EMBO J. 17:1315-1327(1998).
CC -!- SIMILARITY: Belongs to the pp1c/parvulin rotamase family.
DR EMBL; AF035768; AAC49984.1; -.
DR HSSP; Q13526; 1F8A.
DR GO; GO:0016853; P:isomerase activity; IEA.
DR GO; GO:0003755; P:peptidyl-prolyl cis-trans isomerase activity; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR InterPro; IPR000297; Rotamase.
DR InterPro; IPR001202; WW_Rsp5_WMP.
DR Pfam; PF00639; Rotamase; 1.
DR Pfam; PF00397; WW; 1.
DR SMART; SM00456; WW; 1.
DR PROSITE; PS0198; PPIC_PPIASE_2; 1.
DR PROSITE; PS01159; WW_DOMAIN_1; 1.
DR PROSITE; PS0020; WW_DOMAIN_2; 1.
KW Isomerase; Rotamase.
SQ SEQUENCE 176 AA; 20038 MW; 1D1E8376239E1309 CRC64;

Query Match 46.6%; Score 397; DB 2; Length 176;
Best Local Similarity 48.0%; Pred. No. 1.9e-28;
Matches 82; Conservative 24; Mismatches 51; Indels 14; Gaps 2;

QY 7 LPPGWEKMSRSGRVVYFNHITNASQWERPSGNS-----SSGKNGQGEPA-- 53
Db 6 LPAGWEVHSNKNLPYFNPTATRESRWEPPDNTMETLKMVMATYHSGAATYHAPSQE 65
QY 54 -RVRCSHLLVKHSQSRPSRWQEKITRKEALELINGYIQIKSGBEDFESLASQFSD 112
Db 66 GKIRCCHLLVKHRSRRPSSRWREAITRKEAREILRGHQRIMRGELRGDLAMSBD 125
QY 113 CSSAKARGDLGAFSGQMKPFEDASPALRTGEMSGPVFTDGIHIILRTE 163
Db 126 CSSARKKGDLGFGFGEMQAEFEEAFAALPQGVSGIVSGSLHLIERLQ 176

RESULT 15
PIN1_SCHPO STANDARD; PRT; 175 AA.
AC O74448;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Peptidyl-prolyl cis-trans isomerase pin1 (EC 5.2.1.8).
GN Name=pin1; ORFNames=SPCC16C4.03;
OS Schizosaccharomyces pombe (fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360; DOI=10.1038/nature724;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouras J., Feat N., Hayes J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren J., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grynoprez B.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,

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Search completed: April 6, 2005, 06:27:26
Job time : 95 secs